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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,090

DATE: 06/19/2001

TIME: 11:53:14

Input Set : A:\PC9979ASequence.txt

Output Set: N:\CRF3\06192001\I870090.raw

ENTERED

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3 <110> APPLICANT: Pfizer Product Inc.
5 <120> TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
7 <130> FILE REFERENCE: PC9979A
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/870,090
C--> 10 <141> CURRENT FILING DATE: 2001-05-30
12 <150> PRIOR APPLICATION NUMBER: US 60/208,156
13 <151> PRIOR FILING DATE: 2000-05-31
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2749
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (85)..(2700)
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31 agtgcagacg ggcctggggc aggc atg gcg gat tcc agc gaa ggc ccc cgc 111
32 Met Ala Asp Ser Ser Glu Gly Pro Arg
33 1 5
35 gcg ggg ccc ggg gag gtg gct gag ctg ccc ggg gat gag agt ggc acc 159
36 Ala Gly Pro Gly Glu Val Ala Glu Leu Pro Gly Asp Glu Ser Gly Thr
37 10 15 20 25
39 cca ggt ggg gag gct ttt cct ctg tcc tcc ctg gcc aat ctg ttt gag 207
40 Pro Gly Gly Glu Ala Phe Pro Leu Ser Ser Leu Ala Asn Leu Phe Glu
41 30 35 40
43 ggg gag gat ggc tcc ctt tgc ccc tca ccg gct gat gcc agt cgc cct 255
44 Gly Glu Asp Gly Ser Leu Ser Pro Ser Pro Ala Asp Ala Ser Arg Pro
45 45 50 55
47 gct ggc cca ggc gat ggg cga cca aat ctg cgc atg aag ttc cag ggc 303
48 Ala Gly Pro Gly Asp Gly Arg Pro Asn Leu Arg Met Lys Phe Gln Gly
49 60 65 70
51 gcc ttc cgc aag ggg gtg ccc aac ccc atc gat ctg ctg gag tcc acc 351
52 Ala Phe Arg Lys Gly Val Pro Asn Pro Ile Asp Leu Leu Glu Ser Thr
53 75 80 85
55 cta tat gag tcc tgc gtg gtg cct ggg ccc aag aaa gca ccc atg gac 399
56 Leu Tyr Glu Ser Ser Val Val Pro Gly Pro Lys Lys Ala Pro Met Asp
57 90 95 100 105
59 tca ctg ttt gac tac ggc acc tat cgt cac tcc agt gac aac aag 447
60 Ser Leu Phe Asp Tyr Gly Thr Tyr Arg His His Ser Ser Asp Asn Lys
61 110 115 120
63 agg tgg agg aag aag atc ata gag aag cag ccg cag agc ccc aaa gcc 495
64 Arg Trp Arg Lys Lys Ile Ile Glu Lys Gln Pro Gln Ser Pro Lys Ala
65 125 130 135
67 cct gcc cct cag ccg ccc ccc atc ctg aaa gtc ttc aac cgg cct atc 543
68 Pro Ala Pro Gln Pro Pro Pro Ile Leu Lys Val Phe Asn Arg Pro Ile

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71 ctc ttt gac atc gtg tcc cgg ggc tcc act gct gac ctg gac ggg ctg 591
72 Leu Phe Asp Ile Val Ser Arg Gly Ser Thr Ala Asp Leu Asp Gly Leu
73          155          160          165
75 ctc cca ttc ttg ctg acc cac aag aaa cgc cta act gat gag gag ttt 639
76 Leu Pro Phe Leu Leu Thr His Lys Lys Arg Leu Thr Asp Glu Glu Phe
77 170          175          180          185
79 cga gag cca tct acg ggg aag acc tgc ctg ccc aag gcc ttg ctg aac 687
80 Arg Glu Pro Ser Thr Gly Lys Thr Cys Leu Pro Lys Ala Leu Leu Asn
81          190          195          200
83 ctg agc aat ggc cgc aac gac acc atc cct gtg ctg ctg gac atc gcg 735
84 Leu Ser Asn Gly Arg Asn Asp Thr Ile Pro Val Leu Leu Asp Ile Ala
85          205          210          215
87 gag cgc acc ggc aac atg cgg gag ttc att aac tcg ccc ttc cgt gac 783
88 Glu Arg Thr Gly Asn Met Arg Glu Phe Ile Asn Ser Pro Phe Arg Asp
89          220          225          230
91 atc tac tat cga ggt cag aca gcc ctg cac atc gcc att gag cgt cgc 831
92 Ile Tyr Tyr Arg Gly Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg
93          235          240          245
95 tgc aaa cac tac gtg gaa ctt ctc gtg gcc cag gga gct gat gtc cac 879
96 Cys Lys His Tyr Val Glu Leu Leu Val Ala Gln Gly Ala Asp Val His
97 250          255          260          265
99 gcc cag gcc cgt ggg cgc ttc ttc cag ccc aag gat gag ggg ggc tac 927
100 Ala Gln Ala Arg Gly Arg Phe Phe Gln Pro Lys Asp Glu Gly Gly Tyr
101          270          275          280
103 ttc tac ttt ggg gag ctg ccc ctg tcg ctg gct gcc tgc acc aac cag 975
104 Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln
105          285          290          295
107 ccc cac att gtc aac tac cta acg gag aac ccc cac aag aag gcg gac 1023
108 Pro His Ile Val Asn Tyr Leu Thr Glu Asn Pro His Lys Lys Ala Asp
109          300          305          310
111 atg cgg cgc cag gac tcg cga ggc aac aca gtg ctg cat gcg ctg gtg 1071
112 Met Arg Arg Gln Asp Ser Arg Gly Asn Thr Val Leu His Ala Leu Val
113          315          320          325
115 gcc att gct gac aac acc cgt gag aac acc aag ttt gtt acc aag atg 1119
116 Ala Ile Ala Asp Asn Thr Arg Glu Asn Thr Lys Phe Val Thr Lys Met
117 330          335          340          345
119 tac gac ctg ctg ctg ctc aag tgt gcc cgc ctc ttc ccc gac agc aac 1167
120 Tyr Asp Leu Leu Leu Leu Lys Cys Ala Arg Leu Phe Pro Asp Ser Asn
121          350          355          360
123 ctg gag gcc gtg ctc aac aac gac ggc ctc tcg ccc ctc atg atg gct 1215
124 Leu Glu Ala Val Leu Asn Asn Asp Gly Leu Ser Pro Leu Met Met Ala
125          365          370          375
127 gcc aag acg ggc aag att ggg atc ttt cag cac atc atc cgg cgg gag 1263
128 Ala Lys Thr Gly Lys Ile Gly Ile Phe Gln His Ile Ile Arg Arg Glu
129          380          385          390
131 gtg acg gat gag gac aca cgg cac ctg tcc cgc aag ttc aag gac tgg 1311
132 Val Thr Asp Glu Asp Thr Arg His Leu Ser Arg Lys Phe Lys Asp Trp
133          395          400          405

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135 gcc tat ggg cca gtg tat tcc tcg ctt tat gac ctc tcc tcc ctg gac 1359
136 Ala Tyr Gly Pro Val Tyr Ser Ser Leu Tyr Asp Leu Ser Ser Leu Asp
137 410 415 420 425
139 acg tgt ggg gaa gag gcc tcc gtg ctg gag atc ctg gtg tac aac agc 1407
140 Thr Cys Gly Glu Glu Ala Ser Val Leu Glu Ile Leu Val Tyr Asn Ser
141 430 435 440
143 aag att gag aac cgc cac gag atg ctg gct gtg gag ccc atc aat gaa 1455
144 Lys Ile Glu Asn Arg His Glu Met Leu Ala Val Glu Pro Ile Asn Glu
145 445 450 455
147 ctg ctg cgg gac aag tgg cgc aag ttc ggg gcc gtc tcc ttc tac atc 1503
148 Leu Leu Arg Asp Lys Trp Arg Lys Phe Gly Ala Val Ser Phe Tyr Ile
149 460 465 470
151 aac gtg gtc tcc tac ctg tgt gcc atg gtc atc ttc act ctc acc gcc 1551
152 Asn Val Val Ser Tyr Leu Cys Ala Met Val Ile Phe Thr Leu Thr Ala
153 475 480 485
155 tac tac cag ccg ctg gag ggc aca ccg ccg tac cct tac cgc acc acg 1599
156 Tyr Tyr Gln Pro Leu Glu Gly Thr Pro Pro Tyr Pro Tyr Arg Thr Thr
157 490 495 500 505
159 gtg gac tac ctg cgg ctg gct ggc gag gtc att acg ctc ttc act ggg 1647
160 Val Asp Tyr Leu Arg Leu Ala Gly Glu Val Ile Thr Leu Phe Thr Gly
161 510 515 520
163 gtc ctg ttc ttc ttc acc aac atc aaa gac ttg ttc atg aag aaa tgc 1695
164 Val Leu Phe Phe Phe Thr Asn Ile Lys Asp Leu Phe Met Lys Lys Cys
165 525 530 535
167 cct gga gtg aat tct ctc ttc att gat ggc tcc ttc cag ctg ctc tac 1743
168 Pro Gly Val Asn Ser Leu Phe Ile Asp Gly Ser Phe Gln Leu Leu Tyr
169 540 545 550
171 ttc atc tac tct gtc ctg gtg atc gtc tca gca gcc ctc tac ctg gca 1791
172 Phe Ile Tyr Ser Val Leu Val Ile Val Ser Ala Ala Leu Tyr Leu Ala
173 555 560 565
175 ggg atc gag gcc tac ctg gcc gtg atg gtc ttt gcc ctg gtc ctg ggc 1839
176 Gly Ile Glu Ala Tyr Leu Ala Val Met Val Phe Ala Leu Val Leu Gly
177 570 575 580 585
179 tgg atg aat gcc ctt tac ttc acc cgt ggg ctg aag ctg acg ggg acc 1887
180 Trp Met Asn Ala Leu Tyr Phe Thr Arg Gly Leu Lys Leu Thr Gly Thr
181 590 595 600
183 tat agc atc atg atc cag aag att ctc ttc aag gac ctt ttc cga ttc 1935
184 Tyr Ser Ile Met Ile Gln Lys Ile Leu Phe Lys Asp Leu Phe Arg Phe
185 605 610 615
187 ctg ctc gtc tac ttg ctc ttc atg atc ggc tac gct tca gcc ctg gtc 1983
188 Leu Leu Val Tyr Leu Leu Phe Met Ile Gly Tyr Ala Ser Ala Leu Val
189 620 625 630
191 tcc ctc ctg aac ccg tgt gcc aac atg aag gtg tgc aat gag gac cag 2031
192 Ser Leu Leu Asn Pro Cys Ala Asn Met Lys Val Cys Asn Glu Asp Gln
193 635 640 645
195 acc aac tgc aca gtg ccc act tac ccc tcg tgc cgt gac agc gag acc 2079
196 Thr Asn Cys Thr Val Pro Thr Tyr Pro Ser Cys Arg Asp Ser Glu Thr
197 650 655 660 665
199 ttc agc acc ttc ctc ctg gac ctg ttt aag ctg acc att ggc atg ggc 2127

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200 Phe Ser Thr Phe Leu Leu Asp Leu Phe Lys Leu Thr Ile Gly Met Gly
201          670          675          680
203 gac ctg gag atg ctg agc agc acc aag tac ccc gtg gtc ttc atc atc 2175
204 Asp Leu Glu Met Leu Ser Ser Thr Lys Tyr Pro Val Val Phe Ile Ile
205          685          690          695
207 ctg ctg gtg acc tac atc atc ctc acc ttt gtg ctg ctc ctc aac atg 2223
208 Leu Leu Val Thr Tyr Ile Ile Leu Thr Phe Val Leu Leu Leu Asn Met
209          700          705          710
211 ctc att gcc ctc atg ggc gag aca gtg ggc cag gtc tcc aag gag agc 2271
212 Leu Ile Ala Leu Met Gly Glu Thr Val Gly Gln Val Ser Lys Glu Ser
213          715          720          725
215 aag cac atc tgg aag ctg cag tgg gcc acc acc atc ctg gac att gag 2319
216 Lys His Ile Trp Lys Leu Gln Trp Ala Thr Thr Ile Leu Asp Ile Glu
217 730          735          740          745
219 cgc tcc ttc ccc gta ttc ctg agg aag gcc ttc cgc tct ggg gag atg 2367
220 Arg Ser Phe Pro Val Phe Leu Arg Lys Ala Phe Arg Ser Gly Glu Met
221          750          755          760
223 gtc acc gtg ggc aag agc tcg gac ggc act cct gac cgc agg tgg tgc 2415
224 Val Thr Val Gly Lys Ser Ser Asp Gly Thr Pro Asp Arg Arg Trp Cys
225          765          770          775
227 ttc agg gtg gat gag gtg aac tgg tct cac tgg aac cag aac ttg ggc 2463
228 Phe Arg Val Asp Glu Val Asn Trp Ser His Trp Asn Gln Asn Leu Gly
229          780          785          790
231 atc atc aac gag gac ccg ggc aag aat gag acc tac cag tat tat ggc 2511
232 Ile Ile Asn Glu Asp Pro Gly Lys Asn Glu Thr Tyr Gln Tyr Tyr Gly
233          795          800          805
235 ttc tcg cat acc gtg ggc cgc ctc cgc agg gat cgc tgg tcc tcg gtg 2559
236 Phe Ser His Thr Val Gly Arg Leu Arg Arg Asp Arg Trp Ser Ser Val
237 810          815          820          825
239 gta ccc cgc gtg gtg gaa ctg aac aag aac tcg aac ccg gac gag gtg 2607
240 Val Pro Arg Val Val Glu Leu Asn Lys Asn Ser Asn Pro Asp Glu Val
241          830          835          840
243 gtg gtg cct ctg gac agc atg ggg aac ccc cgc tgc gat ggc cac cag 2655
244 Val Val Pro Leu Asp Ser Met Gly Asn Pro Arg Cys Asp Gly His Gln
245          845          850          855
247 cag ggt tac ccc cgc aag tgg agg act gat gac gcc ccg ctc tag 2700
248 Gln Gly Tyr Pro Arg Lys Trp Arg Thr Asp Asp Ala Pro Leu
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251 ggactgcagc ccagccccag cttctctgcc cactcatttc tagtccagc 2749
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255 <211> LENGTH: 871
256 <212> TYPE: PRT
257 <213> ORGANISM: Human
259 <400> SEQUENCE: 2
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261 1 5 10 15
262 Glu Leu Pro Gly Asp Glu Ser Gly Thr Pro Gly Gly Glu Ala Phe Pro
263 20 25 30
264 Leu Ser Ser Leu Ala Asn Leu Phe Glu Gly Glu Asp Gly Ser Leu Ser

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265          35          40          45
266 Pro Ser Pro Ala Asp Ala Ser Arg Pro Ala Gly Pro Gly Asp Gly Arg
267          50          55          60
268 Pro Asn Leu Arg Met Lys Phe Gln Gly Ala Phe Arg Lys Gly Val Pro
269 65          70          75          80
270 Asn Pro Ile Asp Leu Leu Glu Ser Thr Leu Tyr Glu Ser Ser Val Val
271          85          90          95
272 Pro Gly Pro Lys Lys Ala Pro Met Asp Ser Leu Phe Asp Tyr Gly Thr
273          100          105          110
274 Tyr Arg His His Ser Ser Asp Asn Lys Arg Trp Arg Lys Lys Ile Ile
275          115          120          125
276 Glu Lys Gln Pro Gln Ser Pro Lys Ala Pro Ala Pro Gln Pro Pro Pro
277          130          135          140
278 Ile Leu Lys Val Phe Asn Arg Pro Ile Leu Phe Asp Ile Val Ser Arg
279 145          150          155          160
280 Gly Ser Thr Ala Asp Leu Asp Gly Leu Leu Pro Phe Leu Leu Thr His
281          165          170          175
282 Lys Lys Arg Leu Thr Asp Glu Glu Phe Arg Glu Pro Ser Thr Gly Lys
283          180          185          190
284 Thr Cys Leu Pro Lys Ala Leu Leu Asn Leu Ser Asn Gly Arg Asn Asp
285          195          200          205
286 Thr Ile Pro Val Leu Leu Asp Ile Ala Glu Arg Thr Gly Asn Met Arg
287          210          215          220
288 Glu Phe Ile Asn Ser Pro Phe Arg Asp Ile Tyr Tyr Arg Gly Gln Thr
289 225          230          235          240
290 Ala Leu His Ile Ala Ile Glu Arg Arg Cys Lys His Tyr Val Glu Leu
291          245          250          255
292 Leu Val Ala Gln Gly Ala Asp Val His Ala Gln Ala Arg Gly Arg Phe
293          260          265          270
294 Phe Gln Pro Lys Asp Glu Gly Gly Tyr Phe Tyr Phe Gly Glu Leu Pro
295          275          280          285
296 Leu Ser Leu Ala Ala Cys Thr Asn Gln Pro His Ile Val Asn Tyr Leu
297          290          295          300
298 Thr Glu Asn Pro His Lys Lys Ala Asp Met Arg Arg Gln Asp Ser Arg
299 305          310          315          320
300 Gly Asn Thr Val Leu His Ala Leu Val Ala Ile Ala Asp Asn Thr Arg
301          325          330          335
302 Glu Asn Thr Lys Phe Val Thr Lys Met Tyr Asp Leu Leu Leu Leu Lys
303          340          345          350
304 Cys Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val Leu Asn Asn
305          355          360          365
306 Asp Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly Lys Ile Gly
307          370          375          380
308 Ile Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu Asp Thr Arg
309 385          390          395          400
310 His Leu Ser Arg Lys Phe Lys Asp Trp Ala Tyr Gly Pro Val Tyr Ser
311          405          410          415
312 Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu Glu Ala Ser
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VERIFICATION SUMMARY

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DATE: 06/19/2001

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Input Set : A:\PC9979ASequence.txt

Output Set: N:\CRF3\06192001\I870090.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date